WHAT IS CLAIMED IS:

1. In a computer system, a method of identifying an unknown base in a sample nucleic acid sequence, said method comprising the steps of:

inputting a plurality of probe intensities, each of said probe intensities being associated with a nucleic acid probe;

said computer system comparing said plurality of probe intensities wherein each of said plurality of probe intensities is substantially proportional to said associated nucleic acid probe hybridizing with at least one nucleic acid sequence, said at least one nucleic acid sequence including said sample sequence; and

calling said unknown base according to results of said comparing step.

2. In a computer system, a method of identifying an unknown base in a sample nucleic acid sequence, said method comprising the steps of:

inputting a plurality of probe intensities, each of said probe intensities being associated with a nucleic acid probe;

said computer system comparing said plurality of probe intensities wherein each of said plurality of probe intensities is substantially proportional to said associated nucleic acid probe hybridizing with said sample sequence; and

calling said unknown base according to results of said comparing step.

3. The method of claim 2, wherein said comparing step includes the step of said computer system calculating a ratio of a higher probe intensity to a lower probe intensity.

4. The method of claim 3, wherein said calling step includes the step of calling said unknown base according to said probe associated with said higher probe intensity if said ratio is greater than a predetermined ratio value.

5. The method of claim 4, wherein said predetermined ratio value is approximately 1.2.

6. In a computer system, a method of identifying an unknown base in a sample nucleic acid sequence, said method comprising the steps of:

inputting a first set of probe intensities, each of said probe intensities in said first set being associated with a nucleic acid probe and substantially proportional to said associated nucleic acid probe hybridizing with a reference nucleic acid sequence;

inputting a second set of probe intensities, each of said probe intensities in said second set being associated with a nucleic acid probe and substantially proportional to said associated nucleic acid probe hybridizing with said sample sequence;

said computer system comparing at least one of said probe intensities in said first set and at least one of said probe intensities in said second set; and

calling said unknown base according to results of said comparing step.

7. The method of claim 6, wherein said comparing step includes the steps of:

calculating first ratios of a wild-type probe intensity to each probe intensity of a probe hybridizing with said reference sequence, wherein said wild-type probe intensity is associated with a wild-type probe; and

calculating second ratios of the highest probe intensity of a probe hybridizing with said sample sequence to each probe intensity of a probe hybridizing with said sample sequence.

8. The method of claim 7, wherein said comparing step further includes the step of calculating third ratios of said first ratios to said second ratios.

9. The method of claim 8, wherein said calling step includes the step of calling said unknown base according to said probe associated with a highest third ratio.

10. The method of claim 6, wherein said comparing step includes the step of calculating a ratio of a highest probe intensity in said first set to a highest intensity in said second set.

11. The method of claim 10, wherein said comparing step further includes the step of comparing said ratio of neighboring nucleic acid probes.

12. In a computer system, a method of identifying an unknown base in a sample nucleic acid sequence, said method comprising the steps of:

inputting statistics about a plurality of experiments, each of said experiments producing probe intensities each being associated with a nucleic acid probe and substantially proportional to said associated nucleic acid probe hybridizing with a reference nucleic acid sequence;

inputting a plurality of probe intensities, each of said plurality of probe intensities being associated with a nucleic acid probe and substantially proportional to said associated nucleic acid probe hybridizing with said sample sequence;

said computer system comparing at least one of said plurality of probe intensities with said statistics; and

calling said unknown base according to results of said comparing step.

13. The method of claim 12, further comprising the step of calculating said statistics.

14. The method of claim 12, wherein said statistics include a mean and standard deviation.

15. A method of processing first and second nucleic acid sequences, comprising the steps of:

providing a plurality of nucleic acid probes;

labeling said first nucleic acid sequence with a first marker;

labeling said second nucleic acid sequence with a second marker; and

hybridizing said first and second labeled nucleic acid sequences at the same time.

16. The method of claim 15, wherein said plurality of nucleic acid probes are on a chip.

17. The method of claim 15, further comprising the step of fragmenting said first and second nucleic acid sequences at the same time.

18. The method of claim 15, further comprising the step of scanning for said first and second markers on said chip, said first and second labeled nucleic acid sequences being on said chip.

19. The method of claim 15, wherein said first and second markers are fluorescent markers that emit light at different wavelengths upon excitation.

20. In a computer system, a method of identifying mutations in a sample nucleic acid sequence, said method comprising the steps of:

inputting a first set of probe intensities, each of said probe intensities in said first set being associated with a nucleic acid probe and substantially proportional to said associated nucleic acid probe hybridizing with a reference nucleic acid sequence;

inputting a second set of probe intensities, each of said probe intensities in said second set being associated with a nucleic acid probe and substantially proportional to

said associated nucleic acid probe hybridizing with said sample sequence;

said computer system comparing probe intensities in said first set and probe intensities in said second set to select hybridization regions where said probe intensities in said first set and said probe intensities in said second set differ; and

identifying mutations according to characteristics of said selected regions.

21. The method of claim 20, wherein said selected regions are determined by comparing probe intensities of wild-type probes.

22. The method of claim 21, wherein said wild-type probes are complementary to a portion of said reference sequence.

23. The method of claim 21, wherein said identifying step further includes the steps of:

analyzing a size of a selected region;

identifying a likely position of a mutation in said selected region according to an interrogation position of said nucleic acid probes; and

performing base calling at said likely position.

24. In a computer system, a method of analyzing a plurality of sequences of bases, said plurality of sequences including at least one reference sequence and at least one sample sequence, the method comprising the steps of:

displaying said at least one reference sequence in a first area on a display device; and

displaying said at least one sample sequence in a second area on said display device;

whereby a user is capable of visually comparing said plurality of sequences.

25. The method of claim 24, wherein said plurality of sequences are monomer strands of DNA or RNA.

26. The method of claim 24, wherein said at least one reference sequence includes a chip wild-type that has been tiled on a chip.

27. The method of claim 26, wherein said chip wild-type sequence is displayed as a first sequence in said first area.

28. The method of claim 26, further comprising the step of displaying a label in said first area to identify said chip wild-type sequence.

29. The method of claim 24, wherein said at least one sample sequence has been hybridized on a chip.

30. The method of claim 24, further comprising the step of indicating bases that differ among a plurality of user selected sequences.

31. The method of claim 24, further comprising the steps of:

displaying a name associated with each of said at least one reference sequence in said first area; and

displaying a name associated with each of said at least one sample sequence in said second area.

32. The method of claim 24, further comprising the step of linking at least one reference sequence in said first area with at least one sample sequence in said second area.

33. The method of claim 32, further comprising the step of indicating on said display device which sequences are linked.

34. The method of claim 24, further comprising the step of indicating bases of said at least one sample sequence that are not equal to a corresponding base in said at least one reference sequence.

35. The method of claim 24, wherein said at least one reference sequence and said at least one sample sequence are aligned on said display device.
hybridization with said probes.